

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/126,016DATE: 11/03/97  
TIME: 16:58:22

INPUT SET: S21354.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: WALLACH, DAVID  
NOPHAR, YARON  
KEMPER, OLIVER  
ENGELMANN, HARTMUT  
BRAKEBUSCH, CORD  
ADERKA, DAN

(ii) TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
NECROSIS FACTOR BINDING PROTEIN I (TBP-I)

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Browdy and Neimark  
(B) STREET: 419 Seventh Street, N.W., Suite 300  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/126,016  
(B) FILING DATE: 24-SEP-1993  
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 07/625668  
(B) FILING DATE: 13-DEC-1990

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: BROWDY, ROGER L  
(B) REGISTRATION NUMBER: 25,618  
(C) REFERENCE/DOCKET NUMBER: WALLACH4

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 202-628-5197

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/126,016DATE: 11/03/97  
TIME: 16:58:26

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47 (B) TELEFAX: 202-737-3528  
48 (C) TELEX: 248633  
49  
50

51 (2) INFORMATION FOR SEQ ID NO:1:  
52

53 (i) SEQUENCE CHARACTERISTICS:  
54 (A) LENGTH: 2175 base pairs  
55 (B) TYPE: nucleic acid  
56 (C) STRANDEDNESS: single  
57 (D) TOPOLOGY: linear  
58

59 (ii) MOLECULE TYPE: cDNA  
6061 (ix) FEATURE:  
62

63 (A) NAME/KEY: CDS  
64 (B) LOCATION: 256..1620  
65

66 (ix) FEATURE:  
67

68 (A) NAME/KEY: mat\_peptide  
69 (B) LOCATION: 319..1620  
70

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
72

73 CGGCCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA 60  
74  
75 GAAAAATTAAG GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCCC 120  
76  
77 GAGTCTCAAC CCTCAACTGT CACCCCAAGG CACTTGGGAC GTCCTGGACA GACCGAGTCC 180  
78  
79 CGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG 240  
80  
81 CCATAGCTGT CTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG 291  
82 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro  
83 -21 -20 -15 -10  
84  
85 CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT 339  
86 Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile  
87 -5 1 5  
88  
89 GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT 387  
90 Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys  
91 10 15 20  
92  
93 CCC CAA GGA AAA GAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 435  
94 Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr  
95 25 30 35  
96  
97 AAG TGC CAG AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG 483  
98 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly  
99 40 45 50 55

**RAW SEQUENCE LISTING**  
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100																		
101	CAG	GAT	ACG	GAC	TGC	AGG	GAG	TGT	GAG	AGC	GGC	TCC	TTC	ACC	GCT	TCA		531
102	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser		
103					60					65					70			
104																		
105	GAA	AAC	CAC	CTC	AGA	CAC	TGC	CTC	AGC	TGC	TCC	AAA	TGC	CGA	AAG	GAA	579	
106	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu		
107				75					80					85				
108																		
109	ATG	GGT	CAG	GTG	GAG	ATC	TCT	TCT	TGC	ACA	GTG	GAC	CGG	GAC	ACC	GTG	627	
110	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val		
111			90					95					100					
112																		
113	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	TGG	AGT	GAA	AAC	CTT	675	
114	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu		
115		105					110					115						
116																		
117	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG	ACC	GTG	CAC	CTC	723	
118	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu		
119	120					125					130					135		
120																		
121	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC	CAT	GCA	GGT	TTC	771	
122	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe		
123					140					145					150			
124																		
125	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	819	
126	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser		
127				155					160					165				
128																		
129	CTG	GAG	TGC	ACG	AAG	TTG	TGC	CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	867	
130	Leu	Glu	Cys	Thr	Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly		
131			170					175					180					
132																		
133	ACT	GAG	GAC	TCA	GGC	ACC	ACA	GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	915	
134	Thr	Glu	Asp	Ser	Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe		
135		185					190					195						
136																		
137	GGT	CTT	TGC	CTT	TTA	TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	963	
138	Gly	Leu	Cys	Leu	Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr		
139	200					205												

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153	TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC	1155
154	Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr	
155	265 270 275	
156		
157	CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA	1203
158	Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro	
159	280 285 290 295	
160		
161	CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC	1251
162	Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp	
163	300 305 310	
164		
165	CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA	1299
166	Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro	
167	315 320 325	
168		
169	CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC GCC GTG GTG GAG	1347
170	Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu	
171	330 335 340	
172		
173	AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG	1395
174	Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu	
175	345 350 355	
176		
177	AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG	1443
178	Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu	
179	360 365 370 375	
180		
181	CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG	1491
182	Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro	
183	380 385 390	
184		
185	CGG CGC GAG GCC ACG CTG GAG CTG CTG GGA CGC GTG CTC CGC GAC ATG	1539
186	Arg Arg Glu Ala Thr Leu Glu Leu Gly Arg Val Leu Arg Asp Met	
187	395 400 405	
188		
189	GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC	1587
190	Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro	
191	410 415 420	
192		
193	GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGAGGCTGCG CCCTGCGGGC	1640
194	Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg	
195	425 430	
196		
197	AGCTCTAAGG ACCGTCCTGC GAGATCGCCT TCCAACCCCA CTTTTTTCTG GAAAGGAGGG	1700
198		
199	GTCTGCAAGG GGCAAGCAGG AGCTAGCAGC CGCCTACTTG GTGCTAACCC CTGGATGTAC	1760
200		
201	ATAGCTTTTC TCAGCTGCCT GCGCGCCGCC GACAGTCAGC GCTGTGCCCG CGGAGAGAGG	1820
202		
203	TGCGCCGTGG GCTCAAGAGC CTGAGTGGGT GGTGTGCGAG GATGAGGAC GCTATGCCTC	1880
204		
205	ATGCCCGTTT TGGGTGTCCT CACCAGCAAG GCTGCTCGGG GGCCCTGGT TCGTCCCTGA	1940

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/126,016

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206  
207 GCCTTTTTC A CAGTGCATAA GCAGTTTTTT TTGTTTTTGT TTTGTTTTGT TTTGTTTTTA 2000  
208  
209 AATCAATCAT GTTACACTAA TAGAACTTG GCACTCCTGT GCCCTCTGCC TGGACAAGCA 2060  
210  
211 CATAGCAAGC TGAAGTGTCC TAAGGCAGGG GCGAGCACGG AACAAATGGGG CCTTCAGCTG 2120  
212  
213 GAGCTGTGGA CTTTTGTACA TACACTAAAA TTCTGAAGTT AAAAAAAAAA AAAAA 2175  
214  
215

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

226  
227 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
228 -21 -20 -15 -10  
229  
230 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
231 -5 1 5 10  
232  
233 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
234 15 20 25  
235  
236 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
237 30 35 40  
238  
239 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
240 45 50 55  
241  
242 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
243 60 65 70 75  
244  
245 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
246 80 85 90  
247  
248 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
249 95 100 105  
250  
251 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
252 110 115 120  
253  
254 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
255 125 130 135  
256  
257 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
258 140 145 150 155

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**SEQUENCE VERIFICATION REPORT**  
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